SEQUENCE LISTING

<110> Young, John A.T.
      Bradley, Kenneth A.
      Collier, Robert J.
      Mogridge, Jeremy S.

<120> Anthrax Toxin Receptor

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<151> 2000-12-05

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<170> PatentIn Ver. 2.1

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gag cgg aga gcc ctc ggc atc ggc ttc cag tgg ctc tct ttg gcc act 163
Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr
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ctg gtg ctc atc tgc gcc ggg caa ggg gga cgc agg gag gat ggg ggt 211
Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly
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cca gcc tgc tac ggc gga ttt gac ctg tac ttc att ttg gac aaa tca 259
Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser
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gga agt gtg ctg cac cac tgg aat gaa atc tat tac ttt gtg gaa cag 307
Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln
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ttg gct cac aaa ttc atc agc cca cag ttg aga atg tcc ttt att gtt 355
Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val
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Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp Arg Glu
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caa atc cgt caa ggc cta gaa gaa ctc cag aaa gtt ctg cca gga gga       451
Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro Gly Gly
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gac act tac atg cat gaa gga ttt gaa agg gcc agt gag cag att tat       499
Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr
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tat gaa aac aga caa ggg tac agg aca gcc agc gtc atc att gct ttg       547
Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu
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act gat gga gaa ctc cat gaa gat ctc ttt ttc tat tca gag agg gag       595
Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu
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gct aat agg tct cga gat ctt ggt gca att gtt tac tgt gtt ggt gtg       643
Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val Gly Val
165                 170                 175                 180

aaa gat ttc aat gag aca cag ctg gcc cgg att gcg gac agt aag gat       691
Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp
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cat gtg ttt ccc gtg aat gac ggc ttt cag gct ctg caa ggc atc atc       739
His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile
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cac tca att ttg aag aag tcc tgc atc gaa att cta gca gct gaa cca       787
His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro
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tcc acc ata tgt gca gga gag tca ttt caa gtt gtc gtg aga gga aac       835
Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg Gly Asn
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ggc ttc cga cat gcc cgc aac gtg gac agg gtc ctc tgc agc ttc aag       883
Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser Phe Lys
245                 250                 255                 260

atc aat gac tcg gtc aca ctc aat gag aag ccc ttt tct gtg gaa gac       931
Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ser Val Glu Asp
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act tat tta ctg tgt cca gcg cct atc tta aaa gaa gtt ggc atg aaa       979
Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly Met Lys
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gct gca ctc cag gtc agc atg aac gat ggc ctc tct ttt atc tcc agt      1027
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atc gcc ctg ctg atc ctg ttc ctg ctc cta gcc ctg gct ctc ctc tgg    1123
Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp
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tgg ttc tgg ccc ctc tgc tgc act gtg att atc aag gag gtc cct cca    1171
Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val Pro Pro
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ccc cct gcc gag gag agt gag gaa aat aaa ata aaa taacaagaag         1217
Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys
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Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
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Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
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Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
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Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
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Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
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Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
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Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
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Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
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Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
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Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
          180              185          190

Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
          195              200          205

Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
    210              215          220

Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
225              230          235          240

Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
              245          250          255

Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
          260              265          270

Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
          275              280          285

Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
    290              295          300

Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
305              310          315          320

Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
              325          330          335

Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys
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Glu Val Pro Pro Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys
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Leu Asp Ile Gly Pro Arg Gly Asp Arg Val Gly Leu Val Thr Phe Ser
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Ser Asp Ala Arg Val Leu Phe Pro Leu Asn Asp Ser Gln Ser Lys Asp
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Ala Leu Leu Glu Ala Leu Ala Asn Leu Ser Tyr Ser Leu Gly Gly Gly
 65                  70                  75                  80

Thr Asn Leu Gly Ala Ala Leu Glu Tyr Ala Leu Glu Asn Leu Phe Ser
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Glu Ser Ala Gly Ser Arg Arg Gly Ala Pro Lys Val Leu Ile Leu Ile
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Thr Asp Gly Glu Ser Asn Asp Gly Gly Glu Asp Ile Leu Lys Ala Ala
            115                 120                 125

Lys Glu Leu Lys Arg Ser Gly Val Lys Val Phe Val Val Gly Val Gly
            130                 135                 140

Asn Ala Val Asp Glu Glu Glu Leu Lys Lys Leu Ala Ser Ala Pro Gly
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Gly Val Phe Ala Val Glu Asp Leu Pro Glu Leu Leu Asp Leu Leu Ile
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Asp Leu Leu Leu
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Gly Leu Asp Ile Gly Pro Thr Lys Thr Gln Val Gly Leu Ile Gln Tyr
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Ala Asn Asn Pro Arg Val Val Phe Asn Leu Asn Thr Tyr Lys Thr Lys
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Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser Gln Tyr Gly Gly Asp
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Leu Thr Asn Thr Phe Gly Ala Ile Gln Tyr Ala Arg Lys Tyr Ala Tyr
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Val Thr Asp Gly Glu Ser His Asp Gly Ser Met Leu Lys Ala Val Ile
            115                 120                 125

Asp Gln Cys Asn His Asp Asn Ile Leu Arg Phe Gly Ile Ala Val Leu
        130                 135                 140

Gly Tyr Leu Asn Arg Asn Ala Leu Asp Thr Lys Asn Leu Ile Lys Glu
145                 150                 155                 160

Ile Lys Ala Ile Ala Ser Ile Pro Thr Glu Arg Tyr Phe Phe Asn Val
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Ile Phe Ser Ile Glu Gly
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                         1                5                    10

atc ggc ttc cag tgg ctc tct ttg gcc act ctg gtg ctc atc tgc gcc     221
Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala
                15                  20                  25

ggg caa ggg gga cgc agg gag gat ggg ggt cca gcc tgc tac ggc gga     269
Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly
                30                  35                  40

ttt gac ctg tac ttc att ttg gac aaa tca gga agt gtg ctg cac cac     317
Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His
            45                  50                  55
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tgg aat gaa atc tat tac ttt gtg gaa cag ttg gct cac aaa ttc atc      365
Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile
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agc cca cag ttg aga atg tcc ttt att gtt ttc tcc acc cga gga aca      413
Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr
75              80              85              90

acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta      461
Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu
                95              100             105

gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa      509
Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu
            110             115             120

gga ttt gaa agg gcc agt gag cag att tat tat gaa aac aga caa ggg      557
Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly
        125             130             135

tac agg aca gcc agc gtc atc att gct ttg act gat gga gaa ctc cat      605
Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His
        140             145             150

gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat      653
Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp
155             160             165             170

ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca      701
Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr
                175             180             185

cag ctg gcc cgg att gcg gac agt aag gat cat gtg ttt ccc gtg aat      749
Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn
            190             195             200

gac ggc ttt cag gct ctg caa ggc atc atc cac tca att ttg aag aag      797
Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys
            205             210             215

tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga      845
Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly
        220             225             230

gag tca ttt caa gtt gtc gtg aga gga aac ggc ttc cga cat gcc cgc      893
Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg
235             240             245             250

aac gtg gac agg gtc ctc tgc agc ttc aag atc aat gac tcg gtc aca      941
Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr
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ctc aat gag aag ccc ttt tct gtg gaa gat act tat tta ctg tgt cca      989
Leu Asn Glu Lys Pro Phe Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro
        270             275             280
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gcg cct atc tta aaa gaa gtt ggc atg aaa gct gca ctc cag gtc agc     1037
Ala Pro Ile Leu Lys Glu Val Gly Met Lys Ala Ala Leu Gln Val Ser
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atg aac gat ggc ctc tct ttt atc tcc agt tct gtc atc atc acc acc     1085
Met Asn Asp Gly Leu Ser Phe Ile Ser Ser Ser Val Ile Ile Thr Thr
        300             305             310

aca cac tgt tct gac ggt tcc atc ctg gcc atc gcc ctg ctg atc ctg     1133
Thr His Cys Ser Asp Gly Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu
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ttc ctg ctc cta gcc ctg gct ctc ctc tgg tgg ttc tgg ccc ctc tgc     1181
Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys
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Cys Thr Val Ile Ile Lys Glu Val Pro Pro Pro Ala Glu Glu Ser
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gag gaa gaa gat gat gat ggt ctg cct aag aaa aag tgg cca acg gta     1277
Glu Glu Glu Asp Asp Asp Gly Leu Pro Lys Lys Lys Trp Pro Thr Val
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Asp Ala Ser Tyr Tyr Gly Gly Arg Gly Val Gly Gly Ile Lys Arg Met
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gag gtt cgt tgg gga gaa aag ggc tcc aca gaa gaa ggt gct aag ttg     1373
Glu Val Arg Trp Gly Glu Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu
395             400             405             410

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Glu Lys Ala Lys Asn Ala Arg Val Lys Met Pro Glu Gln Glu Tyr Glu
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Pro Arg Lys Trp Tyr Ser Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp
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gtc cta ctg agg aaa gga tat gat cgt gtg tct gtg atg cgt cca cag     1565
Val Leu Leu Arg Lys Gly Tyr Asp Arg Val Ser Val Met Arg Pro Gln
        460             465             470

cca gga gac acg ggg cgc tgc atc aac ttc acc agg gtc aag aac aac     1613
Pro Gly Asp Thr Gly Arg Cys Ile Asn Phe Thr Arg Val Lys Asn Asn
475             480             485             490

cag cca gcc aag tac cca ctc aac aac gcc tac cac acc tcc tcg ccg     1661
Gln Pro Ala Lys Tyr Pro Leu Asn Asn Ala Tyr His Thr Ser Ser Pro
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            525                 530             535

acc ctt ccc cct cct ccc cag gct cca cct ccc aac agg gca cct cct    1805
Thr Leu Pro Pro Pro Pro Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro
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Pro Ser Arg Pro Pro Pro Arg Pro Ser Val
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aaatcaaaaa aaaaaaaaaa aaaaa                                       5540


<210> 6
<211> 564
<212> PRT
<213> Homo sapiens

<400> 6
Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu
 1               5                  10                  15

Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg
            20                  25                  30

Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
        35                  40                  45

Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
    50                  55                  60

Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
65                  70                  75                  80

Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
                85                  90                  95

Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
            100                 105                 110

Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
        115                 120                 125
```

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Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
    130   135   140

Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
145   150   155   160

Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
                165   170   175

Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
                180   185   190

Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
        195   200   205

Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
    210   215   220

Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
225   230   235   240

Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
                245   250   255

Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
                260   265   270

Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
        275   280   285

Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
    290   295   300

Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
305   310   315   320

Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
            325   330   335

Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys
            340   345   350

Glu Val Pro Pro Pro Ala Glu Glu Ser Glu Glu Glu Asp Asp Asp
        355   360   365

Gly Leu Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly
    370   375   380

Gly Arg Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu
385   390   395   400

Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala
                405   410   415

Arg Val Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn
            420   425   430

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```
Leu Asn Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser
        435                 440                 445

Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly
        450                 455                 460

Tyr Asp Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg
465                 470                 475                 480

Cys Ile Asn Phe Thr Arg Val Lys Asn Asn Gln Pro Ala Lys Tyr Pro
                485                 490                 495

Leu Asn Asn Ala Tyr His Thr Ser Ser Pro Pro Pro Ala Pro Ile Tyr
                500                 505                 510

Thr Pro Pro Pro Pro Ala Pro His Cys Pro Pro Pro Pro Ser Ala
        515                 520                 525

Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro
        530                 535                 540

Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro
545                 550                 555                 560

Arg Pro Ser Val
```

<210> 7
<211> 2112
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (113)..(1111)

<400> 7
ggggaataaa ggacccgcga ggaagggccc gcggatggcg cgtccctgag ggtcgtggcg 60

agttcgcgga gcgtgggaag gagcggaccc tgctctcccc gggctgcggg cc atg gcc 118
                                                            Met Ala
                                                             1

```
acg gcg gag cgg aga gcc ctc ggc atc ggc ttc cag tgg ctc tct ttg    166
Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu Ser Leu
         5                  10                  15

gcc act ctg gtg ctc atc tgc gcc ggg caa ggg gga cgc agg gag gat    214
Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg Glu Asp
        20                  25                  30

ggg ggt cca gcc tgc tac ggc gga ttt gac ctg tac ttc att ttg gac    262
Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp
 35                  40                  45                  50
```

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```
aaa tca gga agt gtg ctg cac cac tgg aat gaa atc tat tac ttt gtg      310
Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val
                55                  60                  65

gaa cag ttg gct cac aaa ttc atc agc cca cag ttg aga atg tcc ttt      358
Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe
                70                  75                  80

att gtt ttc tcc acc cga gga aca acc tta atg aaa ctg aca gaa gac      406
Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp
                85                  90                  95

aga gaa caa atc cgt caa ggc cta gaa gaa ctc cag aaa gtt ctg cca      454
Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro
    100                 105                 110

gga gga gac act tac atg cat gaa gga ttt gaa agg gcc agt gag cag      502
Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln
115                 120                 125                 130

att tat tat gaa aac aga caa ggg tac agg aca gcc agc gtc atc att      550
Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile
                    135                 140                 145

gct ttg act gat gga gaa ctc cat gaa gat ctc ttt ttc tat tca gag      598
Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu
                150                 155                 160

agg gag gct aat agg tct cga gat ctt ggt gca att gtt tac tgt gtt      646
Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val
                165                 170                 175

ggt gtg aaa gat ttc aat gag aca cag ctg gcc cgg att gcg gac agt      694
Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
        180                 185                 190

aag gat cat gtg ttt ccc gtg aat gac ggc ttt cag gct ctg caa ggc      742
Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly
195                 200                 205                 210

atc atc cac tca att ttg aag aag tcc tgc atc gaa att cta gca gct      790
Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala
                    215                 220                 225

gaa cca tcc acc ata tgt gca gga gag tca ttt caa gtt gtc gtg aga      838
Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg
                230                 235                 240

gga aac ggc ttc cga cat gcc cgc aac gtg gac agg gtc ctc tgc agc      886
Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser
        245                 250                 255

ttc aag atc aat gac tcg gtc aca ctc aat gag aag ccc ttt tct gtg      934
Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ser Val
    260                 265                 270
```

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```
gaa gat act tat tta ctg tgt cca gcg cct atc tta aaa gaa gtt ggc    982
Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
275                 280                 285                 290

atg aaa gct gca ctc cag gtc agc atg aac gat ggc ctc tct ttt atc   1030
Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile
                    295                 300                 305

tcc agt tct gtc atc atc acc acc aca cac tgt agc ctc cac aaa att   1078
Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Leu His Lys Ile
                310                 315                 320

gca tca ggc ccc aca aca gct gct tgc atg gaa tagcagagaa taccgcctgc  1131
Ala Ser Gly Pro Thr Thr Ala Ala Cys Met Glu
                325                 330

tccctccgga cagcacactc ctgaaaacgg ggagagagga gccaaacatg ctcggtttac  1191

actttcctta tttactgaat gagtggaggg cagagacagg cctggagtta cgcacactga  1251

gtgccccaac atggaaagaa acatcaggag ggacaggaaa cgttccctcc ttaaccaaca  1311

gttttcaaga ccttactgga ggcactttat tggctacata atcactccat gcggtgggca  1371

tcaggcagaa tcctggtgca gacccaactt tgaggtggag gatttcacag tttctttatt  1431

ttgaacttcc cccaggctcc cactaattcc tctccattct atcctcctcc ctttcccaca  1491

aaagaaaaca gaaaggagca gcagtgtttg ataccgtatc atccagaggc ctggttctct  1551

cccattatag ggcaaacaag ccctggcaag atatttcact cccgccccat gccatgcatt  1611

aaaaatccaa aattgcctat attccacctg ccaagcaaga gatgctttca ttattgaagt  1671

tccaaatgta tacctttgag aacagtgcct tctcgtctta aaagagaggt cctcattttg  1731

tgagttggga gcagagggaa ttaaagaaag ccatgatgca gggatttggc cattcaagcc  1791

gggcagcctt cagagaatgt catccctaat gacacatgcc cgaatgaagg agcggggctg  1851

agcttgtcct gccttcgtat tgaatgttgc ctgtctgcct ccttaatagc gggcctctgt  1911

gtgagcattt gacaagactt aaaactattc attgaagaaa atggatgatc ccccaacagg  1971

aagatgcaac cccatgggct gcctgcttga ccacagaagt gcttccagct ccagttgctc  2031

atctgagaac tcccccacc acttgctgtt aaaattgtta aaattaaagg ccatgttgat   2091

tgaaaaaaaa aaaaaaaaa a                                             2112


<210> 8
<211> 333
<212> PRT
<213> Homo sapiens

<400> 8
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-15-

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Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu
 1               5               10              15

Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg
            20              25              30

Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
        35              40              45

Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
    50              55              60

Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
65              70              75              80

Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
            85              90              95

Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
            100             105             110

Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
        115             120             125

Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
    130             135             140

Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
145             150             155             160

Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
            165             170             175

Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
            180             185             190

Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
        195             200             205

Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
    210             215             220

Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
225             230             235             240

Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
            245             250             255

Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
            260             265             270

Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
        275             280             285

Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
    290             295             300
```

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Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Leu His
305                 310                 315                 320

Lys Ile Ala Ser Gly Pro Thr Thr Ala Ala Cys Met Glu
                325                 330




<210> 9
<211> 1436
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (380)..(1033)

<400> 9
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cgcggatggc gcgtccctga gggtcgtggc gagttcgcgg agcgtgggaa ggagcggacc  120

ctgctctccc cgggctgcgg gccatggcca cggcggagcg gagagccctc ggcatcggct  180

tccagtggct ctcacggcca ctctggtgct catctgcgcc gggcaagggg gacgcaggga  240

ggatgggggt ccagcctgct acggcggatt tgacctgtac ttcattttgg acaaatcagg  300

aagtgtgctg caccactgga atgaaatcta ttactttgtg aacagttgg ctcacaaatt  360

catcagccca cagttgagga atg tcc ttt att gtt ttc tcc acc cga gga aca  412
                        Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr
                          1               5                   10

acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta   460
Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu
            15                  20                  25

gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa   508
Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu
        30                  35                  40

gga ttt gaa agg gcc agt gag cag att tat tat gaa aac aga caa ggg   556
Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly
    45                  50                  55

tac agg aca gct agc gtc atc att gct ttg act gat gga gaa ctc cat   604
Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His
60                  65                  70                  75

gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat   652
Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp
                80                  85                  90

ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca   700
Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr
            95                  100                 105
```
-17-

```
cag ctg gcc cgg att gcg gac agt aag gat cat gtg ttt ccc gtg aat    748
Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn
        110                 115                 120

gac ggc ttt cag gct ctg caa ggc atc atc cac tca att ttg aag aag    796
Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys
        125                 130                 135

tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga    844
Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly
140                 145                 150                 155

gag tca ttt caa gtt gtc gtg aga gga aac ggc ttc cga cat gcc cgc    892
Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg
                160                 165                 170

aac gtg gac agg gtc ctc tgc agc ttc aag atc aat gac tcg gtc aca    940
Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr
                175                 180                 185

ctc agt aag tcc ttg cag agt cca tgg gtt tct tcg aca agt ggc ttc    988
Leu Ser Lys Ser Leu Gln Ser Pro Trp Val Ser Ser Thr Ser Gly Phe
            190                 195                 200

aag gaa ggg aat tcc cac cct tgt ctt cca gca agg cca cac aca        1033
Lys Glu Gly Asn Ser His Pro Cys Leu Pro Ala Arg Pro His Thr
            205                 210                 215

tgaaaccagc agaaaagagt cttatttgct ggaaagaccc ccagcaaggg catagtgagc  1093

ccttacagtg gttccagtca gaaaaggcac cacttgggtg ggcacagccc catgggtgtc  1153

caacttggta agcagagcaa ggctggactt gagtccccgt cctccacaaa acacagagcc  1213

acaagcccca gccctgcagc agccctccgg aagcagcggg gcactggttt ccttgtcccc  1273

tgccatctac cgagtggctc actctcaggt gggagtgctg gtgatggtta attaggactg  1333

cagaaacatg agcctcctta acaaagtatt gggactctta agggtaagtg tgaaaaagga  1393

atggtctaaa tgcattaatc ttgaataaac cgaaaaccaa acc                    1436


<210> 10
<211> 218
<212> PRT
<213> Homo sapiens

<400> 10
Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu
 1               5                   10                  15

Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys
             20                  25                  30
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Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala
        35   40   45

Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser
        50   55   60

Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe
65   70   75   80

Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val
                85   90   95

Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile
            100   105   110

Ala Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala
        115   120   125

Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile
        130   135   140

Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val
145   150   155   160

Val Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val
                165   170   175

Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Ser Lys Ser Leu
            180   185   190

Gln Ser Pro Trp Val Ser Ser Thr Ser Gly Phe Lys Glu Gly Asn Ser
        195   200   205

His Pro Cys Leu Pro Ala Arg Pro His Thr
    210   215